RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/611,588A_

Source: _IFWO_

Date Processed by STIC: _5/7/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/611,588A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 _✓_ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IF

```
RAW SEQUENCE LISTING                  DATE: 05/07/2004
PATENT APPLICATION:  US/10/611,588A   TIME: 15:00:48

    Input Set : N:\Crf4\05072004\J611588B.raw
    Output Set: N:\CRF4\05072004\J611588A.raw

 1 <110> APPLICANT: Levanon, et al.
 2 <120> TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
 3 <130> FILE REFERENCE: 10793/70
-> 4 <140> CURRENT APPLICATION NUMBER: US/10/611,588A
 5 <141> CURRENT FILING DATE: 2003-06-30
 6 <150> PRIOR APPLICATION NUMBER: 60/393,491
 7 <151> PRIOR FILING DATE: 2002-07-01
 8 <160> NUMBER OF SEQ ID NOS: 8
 9 <170> SOFTWARE: FastSEQ for Windows Version 3.0
```

pp 1-3

Does Not Comply
Corrected Diskette Needed

```
RORED SEQUENCES

11 <210> SEQ ID NO: 1
12 <211> LENGTH: 280
13 <212> TYPE: PRT
14 <213> ORGANISM: Homo sapiens
15 <400> SEQUENCE: 1
16        Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu
-> 17          5          10          15
18        Ala Ala Gln Pro Ala   Met Ala Glu Val Gln Leu Val Glu Ser Gly
-> 19          20          25          30
20        Gly Gly Val Val Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
-> 21          35          40          45
22        Ala Ser Gly Phe Thr Phe Asp Leu Asn Pro Lys Val Lys His Met
-> 23          50          55          60
24        Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly
-> 25          65          70          75
26        Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
-> 27          80          85          90
28        Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
-> 29          95          100         105
30        Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
-> 31          110         115         120
32        Cys Ala Arg Met Arg Ala Pro Val Ile Trp Gly Gln Gly Thr Leu
-> 33          125         130         135
34        Val Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
-> 35          140         145         150
36        Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser
-> 37          155         160         165
38        Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser
-> 39          170         175         180
40        Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln
```

misaligned
amino acid
numbers.
(see item 3
on Error summary
sheet)

global
error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/611,588A

DATE: 05/07/2004
TIME: 15:00:48

Input Set : N:\Crf4\05072004\J611588B.raw
Output Set: N:\CRF4\05072004\J611588A.raw

```
->  41            185        190      195
    42      Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly
->  43            200        205      210
    44      Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser
->  45            215            220      225
    46      Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr        same
->  47            230                235      240
    48      Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly
->  49            245            250      255
    50      Gly Thr Lys Leu Thr Val Leu Gly Ala Ala Ala Glu Gln Lys Leu
->  51            260            265      270
    52      Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
->  53            275        280
    55  <210> SEQ ID NO: 2
    56  <211> LENGTH: 6
    57  <212> TYPE: PRT
    58  <213> ORGANISM: Homo sapiens                 same
    59  <400> SEQUENCE: 2
    60      Met Arg Ala Pro Val Ile
->  61            5
    63  <210> SEQ ID NO: 3
    64  <211> LENGTH: 16
    65  <212> TYPE: PRT
    66  <213> ORGANISM: Homo sapiens
    67  <400> SEQUENCE: 3
    68      Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
->  69            5                    10    15      same
    71  <210> SEQ ID NO: 4
    72  <211> LENGTH: 8
    73  <212> TYPE: PRT
    74  <213> ORGANISM: Homo sapiens
    75  <400> SEQUENCE: 4
    76      Leu Asn Pro Lys Val Lys His Met        same
->  77            5
    79  <210> SEQ ID NO: 5
    80  <211> LENGTH: 7
    81  <212> TYPE: PRT
    82  <213> ORGANISM: Homo sapiens
    83  <400> SEQUENCE: 5
    84      Leu Arg Gly Gly Asn Ala Met        same
->  85            5
    87  <210> SEQ ID NO: 6
    88  <211> LENGTH: 11
    89  <212> TYPE: PRT
    90  <213> ORGANISM: Homo sapiens
    91  <400> SEQUENCE: 6
    92      Phe Leu Thr Tyr Asn Ser Tyr Glu Val Pro Thr
->  93            5                    10      same
    95  <210> SEQ ID NO: 7
```

RAW SEQUENCE LISTING   DATE: 05/07/2004
PATENT APPLICATION: **US/10/611,588A**   TIME: 15:00:48

Input Set : **N:\Crf4\05072004\J611588B.raw**
Output Set: **N:\CRF4\05072004\J611588A.raw**

```
96 <211> LENGTH: 9
97 <212> TYPE: PRT
98 <213> ORGANISM: Homo sapiens
99 <400> SEQUENCE: 7
100      Thr Asn Trp Tyr Leu Arg Pro Leu Asn
-> 101        5
103 <210> SEQ ID NO: 8
104 <211> LENGTH: 10
105 <212> TYPE: PRT
106 <213> ORGANISM: Homo sapiens
107 <400> SEQUENCE: 8
108      Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
-> 109        5              10
```

same (handwritten, next to line 101)

same (handwritten, next to line 109)

VERIFICATION SUMMARY   DATE: 05/07/2004
PATENT APPLICATION: **US/10/611,588A**   TIME: 15:00:49

Input Set : **N:\Crf4\05072004\J611588B.raw**
Output Set: **N:\CRF4\05072004\J611588A.raw**

1 M:270 C: Current Application Number differs, Wrong Format
17 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
332 Repeated in SeqNo=1
51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
59 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
77 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
85 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
93 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
101 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
109 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8